

0360

#3



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ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/080,233

DATE: 03/13/2002
TIME: 15:11:42

Input Set : A:\GC567-SEQLIST.txt
Output Set: N:\CRF3\03132002\J080233.raw

4 <110> APPLICANT: Wang, Huaming
 6 <120> TITLE OF INVENTION: Novel Phenol Oxidizing Enzymes
 9 <130> FILE REFERENCE: GC567
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/080,233
 C--> 12 <141> CURRENT FILING DATE: 2002-02-19
 14 <160> NUMBER OF SEQ ID NOS: 5
 16 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 1791
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Stachybotrys sp.
 23 <400> SEQUENCE: 1
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 25 ctcggcatcc cgatggacac cggcagccac cccattgagg ctgttgcattcc cgaagtgaag 120
 26 actgagggtct tcgttgactc cttccttgct gcagcaggcg atgacgactg ggagtcaccc 180
 27 ccataacaact tgctttacag gaatgccctg ccaattccac ctgtcaagca gccaaagatg 240
 28 atcattacca accctgtcac cggcaaggac atttggtaact attagatcga gatcaagcca 300
 29 tttcagcaaa ggatttaccc caccttgcgc cctgcactc tcgtcggtcta cgatggcatg 360
 30 agccctggtc ctactttcaa tggcccttgc ggaacagaga ctgttagtttag gttcatcaac 420
 31 aatgccaccg tggagaactc ggtccatctg cacggctccc catcgctgc ccctttcgat 480
 32 gggtgggctg aagatgtgac ctccctggc gagtacaagg attactactt tcccaactac 540
 33 caatccgccc gccttctgtg gtaccatgac cacgtttca tgaagactgc tgagaatgcc 600
 34 tactttggtc aggctggcgc ctacattatac aacgacgagg ctgaggatgc tctcggtctt 660
 35 cctagttggct atggcgagtt cgatataccct ctgatcctga cggccaagta ctataacgcc 720
 36 gatggtaccc tgcgttcgac cgagggttag gaccaggacc tgggggaga tgtcatccat 780
 37 gtcaacggac agccatggcc ttcccttaac gtccagcccc gcaagtaccg ttcccgattc 840
 38 ctcaacgctg ccgtgtctcg tgcttggctc ctctacctcg tcaggaccag ctctcccaac 900
 39 gtcagaattt ctttccaaatg cattgcctct gatgtggtc tccttcaagc ccccggttcag 960
 40 acctctaaccc tctacccctgc tggcccgag cgatcgaga tcattattga cttcaccaac 1020
 41 tttgtggcc agactttga cctgcgcac gttgtcgaga ccaacgatgt cggcgacgag 1080
 42 gatgagtagc ctcgactct cgagggtatcg cgatcgatcg tcagctctgg cactgttgag 1140
 43 gacaacagcc aggtccctc cactctccgt gacgttcctt tccctctca caaggaaggc 1200
 44 cccgcccaca agcacttcaa gttgaacgc agcaacggac actacctgtt caacgatgtt 1260
 45 ggctttggcg atgtcaatga gctgtctcg gccaagcccc agctcgccac cggtgggtc 1320
 46 tgggagctcg agaactccctc tggaggctgg agccaccccg tccacattca ccttggac 1380
 47 ttcaagatcc tcaagcgaac tgggtgtcggt ggccagggtca tgccctacga gtctgttgt 1440
 48 cttttaaggatg tcgtctgggtt gggcagggggt gagaccctga ccatcgaggc ccactaccaa 1500
 49 ccctggactg gagcttacat gtggactgt cacaacctca ttacacggaa taacgacatg 1560
 50 atggctgtat tcaacgtcac cggccatggag gagaagggtt atttcgagga ggacttcgag 1620
 51 gaccccatga accccaatgt ggcgcggcgtt ctttacaacc gcaacgactt ccatgctgc 1680
 52 gctggaaaact tctccggcga gtccatctact gcccggatgc aggagctggc cgagcaggag 1740
 53 ccgtacaacc gcctcgatga gatccctggag gatcttggaa tcgaggagta a 1791
 55 <210> SEQ ID NO: 2

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56 <211> LENGTH: 594
 57 <212> TYPE: PRT
 58 <213> ORGANISM: Stachybotrys sp.
 60 <400> SEQUENCE: 2
 61 Met Leu Phe Lys Ser Trp Gln Leu Ala Ala Ala Ser Gly Leu Leu Ser
 62 1 5 10 15
 63 Gly Val Leu Gly Ile Pro Met Asp Thr Gly Ser His Pro Ile Glu Ala
 64 20 25 30
 65 Val Asp Pro Glu Val Lys Thr Glu Val Phe Ala Asp Ser Leu Leu Ala
 66 35 40 45
 67 Ala Ala Gly Asp Asp Asp Trp Glu Ser Pro Pro Tyr Asn Leu Leu Tyr
 68 50 55 60
 69 Arg Asn Ala Leu Pro Ile Pro Pro Val Lys Gln Pro Lys Met Ile Ile
 70 65 70 75 80
 71 Thr Asn Pro Val Thr Gly Lys Asp Ile Trp Tyr Tyr Glu Ile Glu Ile
 72 85 90 95
 73 Lys Pro Phe Gln Gln Arg Ile Tyr Pro Thr Leu Arg Pro Ala Thr Leu
 74 100 105 110
 75 Val Gly Tyr Asp Gly Met Ser Pro Gly Pro Thr Phe Asn Val Pro Arg
 76 115 120 125
 77 Gly Thr Glu Thr Val Val Arg Phe Ile Asn Asn Ala Thr Val Glu Asn
 78 130 135 140
 79 Ser Val His Leu His Gly Ser Pro Ser Arg Ala Pro Phe Asp Gly Trp
 80 145 150 155 160
 81 Ala Glu Asp Val Thr Phe Pro Gly Glu Tyr Lys Asp Tyr Tyr Phe Pro
 82 165 170 175
 83 Asn Tyr Gln Ser Ala Arg Leu Leu Trp Tyr His Asp His Ala Phe Met
 84 180 185 190
 85 Lys Thr Ala Glu Asn Ala Tyr Phe Gly Gln Ala Gly Ala Tyr Ile Ile
 86 195 200 205
 87 Asn Asp Glu Ala Glu Asp Ala Leu Gly Leu Pro Ser Gly Tyr Gly Glu
 88 210 215 220
 89 Phe Asp Ile Pro Leu Ile Leu Thr Ala Lys Tyr Tyr Asn Ala Asp Gly
 90 225 230 235 240
 91 Thr Leu Arg Ser Thr Glu Gly Glu Asp Gln Asp Leu Trp Gly Asp Val
 92 245 250 255
 93 Ile His Val Asn Gly Gln Pro Trp Pro Phe Leu Asn Val Gln Pro Arg
 94 260 265 270
 95 Lys Tyr Arg Phe Arg Phe Leu Asn Ala Ala Val Ser Arg Ala Trp Leu
 96 275 280 285
 97 Leu Tyr Leu Val Arg Thr Ser Ser Pro Asn Val Arg Ile Pro Phe Gln
 98 290 295 300
 99 Val Ile Ala Ser Asp Ala Gly Leu Leu Gln Ala Pro Val Gln Thr Ser
 100 305 310 315 320
 101 Asn Leu Tyr Leu Ala Val Ala Glu Arg Tyr Glu Ile Ile Ile Asp Phe
 102 325 330 335
 103 Thr Asn Phe Ala Gly Gln Thr Leu Asp Leu Arg Asn Val Ala Glu Thr
 104 340 345 350
 105 Asn Asp Val Gly Asp Glu Asp Glu Tyr Ala Arg Thr Leu Glu Val Met

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106	355	360	365
107	Arg Phe Val Val Ser Ser Gly Thr Val Glu Asp Asn Ser Gln Val Pro		
108	370	375	380
109	Ser Thr Leu Arg Asp Val Pro Phe Pro Pro His Lys Glu Gly Pro Ala		
110	385	390	395
111	Asp Lys His Phe Lys Phe Glu Arg Ser Asn Gly His Tyr Leu Ile Asn		400
112	405	410	415
113	Asp Val Gly Phe Ala Asp Val Asn Glu Arg Val Leu Ala Lys Pro Glu		
114	420	425	430
115	Leu Gly Thr Val Glu Val Trp Glu Leu Glu Asn Ser Ser Gly Gly Trp		
116	435	440	445
117	Ser His Pro Val His Ile His Leu Val Asp Phe Lys Ile Leu Lys Arg		
118	450	455	460
119	Thr Gly Gly Arg Gly Gln Val Met Pro Tyr Glu Ser Ala Gly Leu Lys		
120	465	470	475
121	Asp Val Val Trp Leu Gly Arg Gly Glu Thr Leu Thr Ile Glu Ala His		
122	485	490	495
123	Tyr Gln Pro Trp Thr Gly Ala Tyr Met Trp His Cys His Asn Leu Ile		
124	500	505	510
125	His Glu Asp Asn Asp Met Met Ala Val Phe Asn Val Thr Ala Met Glu		
126	515	520	525
127	Glu Lys Gly Tyr Leu Gln Glu Asp Phe Glu Asp Pro Met Asn Pro Lys		
128	530	535	540
129	Trp Arg Ala Val Pro Tyr Asn Arg Asn Asp Phe His Ala Arg Ala Gly		
130	545	550	555
131	560	565	570
132	Asn Phe Ser Ala Glu Ser Ile Thr Ala Arg Val Gln Glu Leu Ala Glu		
133	575	580	585
134	Gln Glu Pro Tyr Asn Arg Leu Asp Glu Ile Leu Glu Asp Leu Gly Ile		
135	590		
136	Glu Glu		
138	<210> SEQ ID NO: 3		
139	<211> LENGTH: 3677		
140	<212> TYPE: DNA		
141	<213> ORGANISM: Stachybotrys chartarum		
143	<400> SEQUENCE: 3		
144	ctggctagcc tcacttggta gacagccctg acagcctcac tggctggggg tcgaaaggcc	60	
145	agtcaatata ttggtcactg ctaatagttc cttgctacgc gcaaaaagct ccttgcgaa	120	
146	ggggcacaga ctatcaagtg agacatatacg gatgcattgtc tttcatagcc acagtttaggg	180	
147	tggtgaccta ctcgaagagg cccgacttg catgcatacg acatgtcgct tccatgcaac	240	
148	atgtatgcgc acatccgcga tcagggcaccc tctgcatgca gaatagaacc cccctgggtt	300	
149	ccttttgtt cttttccctt ctcaacgcacg cgtgagcgtg gttacttga gcaaggccga	360	
150	gtggtctgtt cacgaggtt ccattcgaact ctcttcttc ccaatcatga cctgcccccc	420	
151	gagtttagcc cccatcacgg ctgtgaaatc cacttcgata atccttagcct agtgcactc	480	
152	ttcaatagtt gtcctgtatg gggcactttg gtcacattgc cttggattyct ctcacctcg	540	
153	tctcttccgc atcaaggctc tatgcccgcac gacaacacct cattggcccg gaccactttg	600	
154	agcgcgcacg caccttcgcg ccgaaggagt tgataaacacc cttcaccctt gcccaatgtat	660	
155	ggagttttgg tctatttgc atgatcacct cacattcaact agatcacggta tccttggaaaga	720	
156	gggtgtggaa gccagaccag cttgtccctg ttcttgcaga ctcaggtcag ctcctagcgg	780	
157	ctatcacagc tcaggattat caagtcccgtaa aagttccaga ccctttcat tgtatgtat	840	

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158	tgcctaattt	gcgctatctc	tatgccgtag	cagccgtctt	ggctacaact	ggctgccatg	900
159	gctgaagcat	cgtgagatct	ataaaggctct	ccgaatccctc	ggtgaagtca	gaatcgctc	960
160	tccacaccag	tcaacaacaa	gcttcttct	cttacagctt	agcctgagca	cattcacaga	1020
161	actcttcctt	tctttcgctc	aatatgttgt	tcaagtcatg	gcaactggca	gcagcctccg	1080
162	ggctcctgtc	tggagtccctc	ggcatcccg	tggacaccgg	cagccacccc	attgaggctg	1140
163	ttgatcccg	agtgaagact	gaggtcttcg	ctgactccct	ccttgcgtca	gcagggcgatg	1200
164	acgactggga	gtcacctcca	tacaacttgc	tttacaggtg	agacacctgt	cccacctgtt	1260
165	ttccctcgat	aactaactct	tataggaatg	ccctgccaat	tccacctgtc	aagcagccca	1320
166	agatgtatgt	ctttgatttt	ctacgaagca	actcggcccc	gactaatgt	ttcttaggatc	1380
167	attaccaacc	ctgtcaccgg	caaggacatt	tggtactatg	agatcgagat	caagccattt	1440
168	cagcaaagg	tgagttgtc	cagaaaccc	gtggtaatta	atcattgtt	ctgacccttt	1500
169	cagatttacc	ccacccgtcg	ccctgccaact	ctcgctggct	acgatggcat	gagccctgg	1560
170	cctactttca	atgttcccg	aggaacagag	actgttagtta	ggttcatcaa	caatgccacc	1620
171	gtggagaact	cggtccatct	gcacggctcc	ccatcgctg	ccccttcga	tggggggct	1680
172	gaagatgtga	ccttccctgg	cgagtacaag	gattactact	ttcccaacta	ccatccgccc	1740
173	cgcctctgt	ggtaccatga	ccacgcttcc	atgaaggat	gctacgagcc	tttatcttcc	1800
174	ttggctacct	ttggctaacc	aacttcctt	cgtagactgc	tgagaatgcc	tacttgg	1860
175	aggctggcg	ctacattatc	aacgacgagg	ctgaggatgc	tctcggtctt	cctagtggct	1920
176	atggcgagtt	cgatatccct	ctgatcctga	cgccaagta	ctataacgcc	gatggta	1980
177	tgcgttcgac	cgagggtgag	gaccaggacc	tgtgggaga	tgtcatccat	gtcaacggac	2040
178	agccatggcc	tttccttaac	gtccagcccc	gcaagtaccg	ttccgattt	ctcaacgctg	2100
179	cctgtctcg	tgcttggctc	ctctacctcg	tcaggaccag	ctctccaa	gtcagaattc	2160
180	cttccaagt	cattgcctc	gatgctggc	tccttcaagc	ccccgttcag	acctctaacc	2220
181	tctacccgtc	tgttggccag	cttacgaga	tcattattgg	tatgccctcc	cctctcacga	2280
182	atgagtcaag	aactctaaga	ctaacacttgc	tagacttcac	caactttgt	ggccagactc	2340
183	ttgacccgtc	caacgttgc	gagaccaacg	atgtccgcga	cgaggatgag	tacgctcgca	2400
184	ctctcgaggt	gatgcgttcc	gtcgctcag	ctggactgt	tgaggacaac	agccagggtcc	2460
185	cctccactct	ccgtgacgtt	ccttccttc	ctcacaagga	aggccccccc	gacaaggact	2520
186	tcaagttga	acgcagcaac	ggacactacc	tgatcaacga	tgttggctt	gccgatgtca	2580
187	atgagcgtgt	cctggccaag	cccgagctcg	gcaccgtga	ggtctggag	ctcgagaact	2640
188	cctctggagg	ctggagccac	cccggtccaca	ttcaccttgc	tgacttcaag	atcctcaagc	2700
189	gaactgggt	tcgtggccag	gtcatgcct	acgagtctgc	tggcttaag	gatgtcgct	2760
190	ggttggccag	gggtgagacc	ctgaccatcg	aggccacta	ccaaccctgg	actggagctt	2820
191	acatgtggca	ctgtacacaac	ctcatttcacg	aggataacga	catgatgct	gtattcaacg	2880
192	tcaccgcct	ggaggagaag	ggtatcttc	aggaggactt	cgaggacccc	atgaacccca	2940
193	agtggcgccg	cgttccat	aaccgcaacg	acttccatgc	tcgcgctg	aacttctccg	3000
194	ccgagtcat	cactggccga	gtgcaggagc	tggccgagca	ggagccgtac	aaccgcctcg	3060
195	atgagatcc	ggaggatctt	gaaatcgagg	agtaaacc	gagccacaag	ctctacaatc	3120
196	gttttgcgtc	ttaagacgag	gcttgcgtt	cgtattctt	tcttcctac	ggggactcc	3180
197	gctgtccact	gcgtatgtaa	ggaccatcac	aaagcaacgt	atataattgg	ctcaccactg	3240
198	tcattaccgc	ccacttgtac	ctattcgatt	cttgcgtaaa	ctttctgt	gctgagatgt	3300
199	ccatagtcaa	gaaacccca	tagggctatc	gtctaaactg	aactattgt	tggctgtga	3360
200	cgtggagtag	atgtcaattt	tgtgagaca	cagtaaatac	ggtatatctt	ttccttaggac	3420
201	tacaggatca	gttttcat	agattacatc	cgtctaattgt	ttgtccatga	gagtcgt	3480
202	aagggttgg	atgcatacaga	cgaaatcatt	tgatgcgtc	agtcgtatt	accgatgtaa	3540
203	gacaagtttag	gtaagttgtc	tggatcccg	aaatgactca	ggctccctca	ttaggttgc	3600
204	tgtaaaacc	ttcagcaact	catgggttt	gggaccaa	atccatacc	tgatgttgc	3660
205	aactgacctg	ggtcaat					3677
207	<210>	SEQ ID NO:	4				

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Input Set : A:\GC567-SEQLIST.txt
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208 <211> LENGTH: 568
 209 <212> TYPE: PRT
 210 <213> ORGANISM: Bilirubin oxidase
 212 <400> SEQUENCE: 4
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 216 20 25 30
 217 Gly His Leu Phe Lys Arg Val Ala Gln Ile Ser Pro Gln Tyr Pro Met
 218 35 40 45
 219 Phe Thr Val Pro Leu Pro Ile Pro Pro Val Lys Gln Pro Arg Leu Thr
 220 50 55 60
 221 Val Thr Asn Pro Val Asn Gly Gln Glu Ile Trp Tyr Tyr Glu Val Glu
 222 65 70 75 80
 223 Ile Lys Pro Phe Thr His Gln Val Tyr Pro Asp Leu Gly Ser Ala Asp
 224 85 90 95
 225 Leu Val Gly Tyr Asp Gly Met Ser Pro Gly Pro Thr Phe Gln Val Pro
 226 100 105 110
 227 Arg Gly Val Glu Thr Val Val Arg Phe Ile Asn Asn Ala Glu Ala Pro
 228 115 120 125
 229 Asn Ser Val His Leu His Gly Ser Phe Ser Arg Ala Ala Phe Asp Gly
 230 130 135 140
 231 Trp Ala Glu Asp Ile Thr Glu Pro Gly Ser Phe Lys Asp Tyr Tyr Tyr
 232 145 150 155 160
 233 Pro Asn Arg Gln Ser Ala Arg Thr Leu Trp Tyr His Asp His Ala Met
 234 165 170 175
 235 His Ile Thr Ala Glu Asn Ala Tyr Arg Gly Gln Ala Gly Leu Tyr Met
 236 180 185 190
 237 Leu Thr Asp Pro Ala Glu Asp Ala Leu Asn Leu Pro Ser Gly Tyr Gly
 238 195 200 205
 239 Glu Phe Asp Ile Pro Met Ile Leu Thr Ser Lys Gln Tyr Thr Ala Asn
 240 210 215 220
 241 Gly Asn Leu Val Thr Thr Asn Gly Glu Leu Asn Ser Phe Trp Gly Asp
 242 225 230 235 240
 243 Val Ile His Val Asn Gly Gln Pro Trp Pro Phe Lys Asn Val Glu Pro
 244 245 250 255
 245 Arg Lys Tyr Arg Phe Arg Phe Leu Asp Ala Ala Val Ser Arg Ser Phe
 246 260 265 270
 247 Gly Leu Tyr Phe Ala Asp Thr Asp Ala Ile Asp Thr Arg Leu Pro Phe
 248 275 280 285
 249 Lys Val Ile Ala Ser Asp Ser Gly Leu Leu Glu His Pro Ala Asp Thr
 250 290 295 300
 251 Ser Leu Leu Tyr Ile Ser Met Ala Glu Arg Tyr Glu Val Val Phe Asp
 252 305 310 315 320
 253 Phe Ser Asp Tyr Ala Gly Lys Thr Ile Glu Leu Arg Asn Leu Gly Gly
 254 325 330 335
 255 Ser Ile Gly Gly Ile Gly Thr Asp Thr Asp Tyr Asp Asn Thr Asp Lys
 256 340 345 350
 257 Val Met Arg Phe Val Val Ala Asp Asp Thr Thr Gln Pro Asp Thr Ser

VERIFICATION SUMMARY

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Input Set : A:\GC567-SEQLIST.txt

Output Set: N:\CRF3\03132002\J080233.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date